

# **THE USE OF DATA WAREHOUSING AND ONLINE ANALYTICAL PROCESSING (OLAP) TO IDENTIFY RESISTANCE GENES AND PATHWAYS IN A RESISTANT SOYBEAN CULTIVAR (PEKING) AGAINST THE CYST NEMATODE.**

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Changes in gene expression in roots of soybean, cv. Peking, resistant to attack by the soybean cyst nematode (SCN), *Heterodera glycines*, at 6, 12 and 24 hours, 2, 4, 6, and 8 days post invasion were monitored using microarrays containing over 6,000 cDNA inserts. Replicate, independent biological samples were examined at each time point. We used database warehousing and online analytical processing (OLAP) in conjunction with statistical database applications to analyze the gene expression data. OLAP was used as a data mining tool to quickly and efficiently find patterns and biological insights into the resistance pathways of soybean against SCN. OLAP was found to supplement cluster analysis and discover new candidate resistance genes that cluster analysis did not. The salicylic acid (SA) inducible genes PR-1a and NPR1 were found to be statistically induced using T-tests and OLAP. The induction of the SA defense pathway leads to the resistance against a wide range of pathogens and parasites in a number of plant species. Jasmonic acid (JA) inducible genes were also induced, these included lipoxygenase, chalcone synthase and PR-6. Other candidate resistance genes that were found induced were ubiquitin, glutathione s-transferase (GST) and aquaporin, all of which are involved in the systematic defense mechanism of plants against pathogen attack. Our results suggest that a combination of different defense related pathways, including the SA and JA inducible pathways, are joined together to tailor a response in Peking that confers its resistance to SCN.